GENETIC AND ENVIRONMENTAL CHARACTERISTICS OF ISOLATED COASTAL CUTTHROAT TROUT POPULATIONS

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Introduction

Threats to the persistence of small populations include genetic, demographic, and environmental factors, but few studies have examined the relationship between these factors or their relative importance. To explore the interaction of these factors through ecological time, and their impact on small natural populations, we are studying coastal cutthroat trout (*Oncorhynchus clarki clarki*) from above and below waterfalls created by isostatic rebound. Understanding how naturally isolated populations persist and maintain genetic variability is critical to conservation efforts for the multitude of species now suffering from habitat degradation and fragmentation.

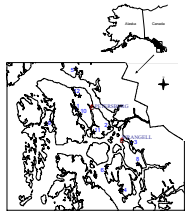
Southeastern Alaska was almost completely covered by ice during the late Pleistocene. Glaciation, and subsequent inundation by seawater following the retreat of the icesheet, produced a highly fragmented landscape of islands and fjords with numerous small streams leading directly to saltwater. Available evidence suggests that anadromous salmonids generally colonized the lower reaches of these streams within decades of glacial retreat. During the early Holocene period (about 10,000 years ago), isostatic rebound revealed waterfalls on many streams, leaving fish trapped above them. These now freshwater-resident salmonid populations have since been isolated without the possibility of immigration or recolonization, offering the rare opportunity to study the persistence of isolated populations over thousands of generations in a natural setting.

Migration barrier.

Typical habitat at study sites.

Methods

- Using GIS-based topographic data for southeastern Alaska, we identified permanent, natural upstream movement barriers (waterfalls).
- We selected 12 streams with visually confirmed barriers that harbor coastal cutthroat trout above them and have large variation in the amount of available upstream habitat (1.5-35 km).
- Above-barrier census population sizes (N) were estimated by multiplying habitat length by the estimated average above-barrier adult fish density (determined by intensive sampling at multiple representative test sites).
- Tissue samples from approximately 30 individuals were collected both above and below the barriers in eight of the streams (Sites 1-8), and above-barrier samples only were collected in the other four streams (Sites 9-12).



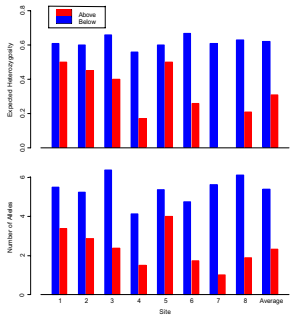
Sampling sites.

- Eight microsatellite loci were used to estimate genetic variability within and among the 20 collections.
- Estimates of effective population size (Ne) were calculated from the reduction in heterozygosity observed between collections above and below (assumed as founding level at isolation) each barrier; 2500 generations assumed.

Results

Within Population Variability

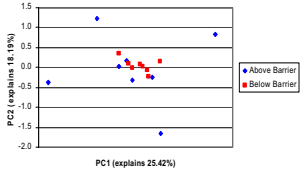
- Genetic variability measured by expected heterozygosity and average number of alleles per locus over eight microsatellite loci, is much lower in the above barrier collections than it is below barriers for all eight paired sites.
- Average expected heterozygosity is 0.62 below barriers and 0.31 above barriers.
- Average number of alleles per locus is 5.4 below barriers and 2.3 above barriers.



Genetic variability above and below barriers.

Among Population Variability

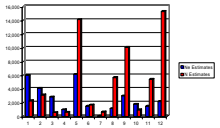
- Significant allele frequency differences were detected among all pairwise comparisons for the 20 collections at each locus and over all loci ($p<0.0001$).
- Overall F_{ST} values are 0.10 for the eight below barrier populations, and 0.57 for the 12 above barrier populations.



Principal component analysis of genetic variability.

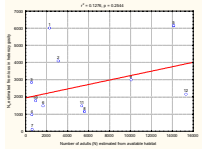
- The pattern of genetic variation reflects the random effects of genetic drift driving the above barrier collections apart, and the homogenizing effects of gene flow, albeit limited, in the below barrier collections.
- One-way gene flow downstream is evident. Based on their multilocus genotypes, some individuals captured at several below barrier sites obviously belonged to the above barrier populations, but had passed downstream over the barriers. These individuals were not excluded from analysis; genetic differences shown here are therefore represent minimum values.

Genetic Diversity and Habitat Size



Estimates of Ne and N.

- For the 12 above barrier populations, estimates of adult population sizes inferred from habitat area (used here as a surrogate for N) and effective population sizes calculated from observed reduction in heterozygosity (used here as a surrogate for Ne) show similar trends and average 3,000-5,000 spawning adults.



Regression of Ne on N.

- Correlations between these estimates are evident, but weak, indicating that the relationship between habitat size and the maintenance of genetic variability is not strictly linear and that other factors are involved.

Conclusions and Future Direction

- Our results: 1) confirm previous studies indicating that coastal cutthroat trout populations are structured at small geographic scales and should be managed as such; and 2) qualitatively support theoretical predictions for loss of genetic diversity in isolated populations.
- Quantitatively, the loss of genetic diversity observed seems to be less than expected, indicating there are more complex interactions of variables maintaining the variation in these isolated populations warranting further study.
- The weak correlation between the amount of available habitat and genetic estimates of Ne also indicates there are other factors influencing this interaction.
- While genetic variability is significantly reduced in the above barrier populations, these completely isolated and relatively small populations have persisted for thousands of generations and appear healthy.
- Continued investigation into the genetic and environmental forces acting on naturally isolated populations are needed to direct conservation efforts for small and isolated populations.
- Factors we plan to study next include age-structure, breeding strategy, in reach movement and the potential presence of multiple populations within the small and steep reaches above barriers.

Acknowledgements

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